In the specification:

Please replace the paragraph at page 6, line 15, with the following:

Panel a: Diagrammatic representation of two tTA proteins. In both fusion proteins, tTA and tTA_S, the original 207-amino-acid sequence of tetR is conserved. Two versions of VP 16 sequences encoding the activation domain were fused in frame to the 3' end of the tetR gene, resulting in tTA and tTAs. The bold letters indicate the original amino acids at the N terminal end, the junction (SEQ ID NOs: 11 and 12), and the C-terminal end of the fusion proteins (SEQ ID NO: 13); the other letters designate amino acids introduced due to sequence constraints of the particular system. The numbers delineate amino acid positions within tetR (Hillen and Wissman in Protein-Nucleic Acid Interaction, Topics in Molecular and Structural Biology, Saenger and Heinemann (eds.), Vol 10, pp. 143-162 (1989)) or VP16 (Treizenberg et al., Genes Dev. 2:718-729 (1988)), respectively.

Please replace the paragraph at page 6, line 25, with the following:

Panel b: The tTA-dependent transcriptional unit consists of the simian virus 40 (SV40) poly(A) site (An), the luciferase gene (luc), the P_{hCMV}*-l or P_{hCMV}*-2. The two promoters encompass the sequence between +75 and -53 of the P_{hCMV}*-2 with one base-pair exchange at -31, which creates a Stu I cleavage site (SEQ ID NO: 15). The Xho I site (SEQ IDNO:16) introduced at -53 by PCR was utilized to insert the heptamerized tetO sequence (SEQ ID NOs: 14 and 17). This heptameric sequence is flanked at one side by an 18-nucleotide polylinker, which allows the insertion of the operators in both orientations as Sal l/Xhol fragments. The position of the central G/C base pair of the promoter proximal operator to position +l is -95 for P_{hCMV}*-I (upper construct) and -76 for P_{hCMV}*-2 (lower construct). The plasmids that contain the four constructs are indicated on the far right.